

OIPE

RAW SEQUENCE LISTING

DATE: 10/24/2001

PATENT APPLICATION: US/09/903,216

TIME: 15:12:30

Input Set : A:\Rih32d21.app

Output Set: N:\CRF3\10242001\I903216.raw

3 <110> APPLICANT: Wands, Jack R.
4 de la Monte, Suzanne M.
5 Ince, Nedim
6 Carlson, Rolf I.
8 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
10 <130> FILE REFERENCE: 21486-032 DIV2
12 <140> CURRENT APPLICATION NUMBER: 09/903,216
13 <141> CURRENT FILING DATE: 2001-07-11
15 <150> PRIOR APPLICATION NUMBER: 09/436,184
16 <151> PRIOR FILING DATE: 1999-11-08
18 <160> NUMBER OF SEQ ID NOS: 9
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 36
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
29 EGF-like domain
31 <220> FEATURE:
32 <221> NAME/KEY: VARIANT
33 <222> LOCATION: (2)..(8)
34 <223> OTHER INFORMATION: Wherein Xaa is any amino acid
36 <220> FEATURE:
37 <221> NAME/KEY: VARIANT
38 <222> LOCATION: (10)..(13)
39 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
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42 <221> NAME/KEY: VARIANT
43 <222> LOCATION: (15)..(24)
44 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
46 <220> FEATURE:
47 <221> NAME/KEY: VARIANT
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49 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
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52 <221> NAME/KEY: VARIANT
53 <222> LOCATION: (28)..(35)
54 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
56 <400> SEQUENCE: 1
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58 1 5 10 15
W--> 60 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa
61 20 25 30
W--> 63 Xaa Xaa Xaa Cys
64 35
67 <210> SEQ ID NO: 2

ENTERED

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68 <211> LENGTH: 758

69 <212> TYPE: PRT

70 <213> ORGANISM: Homo sapiens

72 <400> SEQUENCE: 2

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74   1      5      10      15
76 Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala
77      20      25      30
79 Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly
80      35      40      45
82 Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu
83      50      55      60
85 Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr
86      65      70      75      80
88 Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly
89      85      90      95
91 Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg
92      100     105     110
94 Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr
95      115     120     125
97 Glu Pro Glu Glu Gln Val Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
98      130     135     140
100 Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His
101 145      150      155      160
103 Ala Glu His Val Glu Gly Glu Asp Leu Gln Glu Asp Gly Pro Thr
104      165     170     175
106 Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val
107      180     185     190
109 Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr
110      195     200     205
112 Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln
113      210     215     220
115 Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu
116 225      230      235      240
118 Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr
119      245     250     255
121 Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu
122      260     265     270
124 Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val
125      275     280     285
127 Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu
128      290     295     300
130 Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro
131 305      310      315      320
133 Glu Gln Lys Ala Lys Val Lys Lys Lys Lys Pro Lys Leu Leu Asn Lys
134      325     330     335
136 Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg
137      340     345     350
139 Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val

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140	355	360	365
142 Arg Lys Tyr Pro Gln Ser	Pro Arg Ala Arg Tyr Gly	Lys Ala Gln Cys	
143 370	375	380	
145 Glu Asp Asp Leu Ala Glu	Lys Arg Arg Ser Asn	Glu Val Leu Arg Gly	
146 385	390	395	400
148 Ala Ile Glu Thr Tyr Gln	Glu Val Ala Ser Leu	Pro Asp Val Pro Ala	
149 405	410	415	
151 Asp Leu Leu Lys Leu Ser	Leu Lys Arg Arg Ser	Asp Arg Gln Gln Phe	
152 420	425	430	
154 Leu Gly His Met Arg Gly	Ser Leu Leu Thr Leu	Gln Arg Leu Val Gln	
155 435	440	445	
157 Leu Phe Pro Asn Asp Thr	Ser Leu Lys Asn Asp	Leu Gly Val Gly Tyr	
158 450	455	460	
160 Leu Leu Ile Gly Asp Asn	Asp Asn Ala Lys Lys	Val Tyr Glu Glu Val	
161 465	470	475	480
163 Leu Ser Val Thr Pro Asn	Asp Gly Phe Ala Lys	Val His Tyr Gly Phe	
164 485	490	495	
166 Ile Leu Lys Ala Gln Asn	Lys Ile Ala Glu Ser	Ile Pro Tyr Leu Lys	
167 500	505	510	
169 Glu Gly Ile Glu Ser Gly	Asp Pro Gly Thr Asp	Asp Gly Arg Phe Tyr	
170 515	520	525	
172 Phe His Leu Gly Asp Ala	Met Gln Arg Val Gly	Asn Lys Glu Ala Tyr	
173 530	535	540	
175 Lys Trp Tyr Glu Leu Gly	His Lys Arg Gly His	Phe Ala Ser Val Trp	
176 545	550	555	560
178 Gln Arg Ser Leu Tyr Asn	Val Asn Gly Leu Lys	Ala Gln Pro Trp Trp	
179 565	570	575	
181 Thr Pro Lys Glu Thr Gly	Tyr Thr Glu Leu Val	Lys Ser Leu Glu Arg	
182 580	585	590	
184 Asn Trp Lys Leu Ile Arg	Asp Glu Gly Leu Ala	Val Met Asp Lys Ala	
185 595	600	605	
187 Lys Gly Leu Phe Leu Pro	Glu Asp Glu Asn Leu	Arg Glu Lys Gly Asp	
188 610	615	620	
190 Trp Ser Gln Phe Thr Leu	Trp Gln Gln Gly Arg	Arg Asn Glu Asn Ala	
191 625	630	635	640
193 Cys Lys Gly Ala Pro Lys	Thr Cys Thr Leu Leu	Glu Lys Phe Pro Glu	
194 645	650	655	
196 Thr Thr Gly Cys Arg Arg	Gly Gln Ile Lys Tyr	Ser Ile Met His Pro	
197 660	665	670	
199 Gly Thr His Val Trp Pro	His Thr Gly Pro Thr	Asn Cys Arg Leu Arg	
200 675	680	685	
202 Met His Leu Gly Leu Val	Ile Pro Lys Glu Gly	Cys Lys Ile Arg Cys	
203 690	695	700	
205 Ala Asn Glu Thr Arg Thr	Trp Glu Glu Gly Lys	Val Leu Ile Phe Asp	
206 705	710	715	720
208 Asp Ser Phe Glu His Glu	Val Trp Gln Asp Ala	Ser Ser Phe Arg Leu	
209 725	730	735	
211 Ile Phe Ile Val Asp Val	Trp His Pro Glu Leu	Thr Pro Gln Gln Arg	
212 740	745	750	

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214 Arg Ser Leu Pro Ala Ile

215 755

218 <210> SEQ ID NO: 3

219 <211> LENGTH: 2324

220 <212> TYPE: DNA

221 <213> ORGANISM: Homo sapiens

223 <400> SEQUENCE: 3

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225 gctccggcag cggtagcacg agtgcgggca gcagcagccc cggggcccgg agagagacaa 120
226 agcatggagg acacaagaat gggaggaaa ggcgactctc gggaacttca ttcttcacgt 180
227 ggtttatggt gattgcattg ctgggcgtct ggacatctgt agctgtcgtt tggtttgatc 240
228 ttgttgacta tgaggaaagt ctaggaaaac taggaatcta tgatgctgat ggtgatggag 300
229 attttgatgt ggatgatgcc aaagttttat taggacttaa agagagatct acttcagagc 360
230 cagcagtccc gccagaagag gctgagccac acactgagcc cgaggagcag gttcctgtgg 420
231 aggcagaacc ccagaatata gaagatgaag caaaagaaca aattcagtc cttctccatg 480
232 aaatggtaca cgcagaacat gttgagggag aagacttgca acaagaagat ggaccacag 540
233 gagaaccaca acaagaggat gatgagtttc ttatggcgac tgatgtagat gatagatttg 600
234 agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtggaagaga 660
235 cagtttcaca agactgtaat caggatatgg aagagatgat gtctgagcag gaaaatccag 720
236 attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtaacat 780
237 accaagtcta tgaggaacaa gcagtatatg aacctctaga aaatgaaggg atagaaatca 840
238 cagaagtaac tgctccccct gaggataatc ctgtagaaga ttcacaggta attgtagaag 900
239 aagtaagcat ttttcctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaa 960
240 cagatgatcc agaacaaaaa gcaaaagtta agaaaaagaa gcctaaactt ttaaataaat 1020
241 ttgataagac tattaaagct gaacttgatg ctgcagaaaa actccgtaaa aggggaaaaa 1080
242 ttgaggaagc agtgaatgca tttaaagaac tagtacgcaa ataccctcag agtccacgag 1140
243 caagatatgg gaaggcgagc tgtgaggatg atttggctga gaagaggaga agtaatgagg 1200
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258 ggccgcacac agggcccaca aactgcaggc tccgaatgca cctgggcttg gtgattccca 2100
259 aggaaggctg caagattcga tgtgccaacg agaccaggac ctgggaggaa ggcaagggtg 2160
260 tcattcttga tgactccttt gagcacgagg tatggcagga tgacctatct ttccggctga 2220
261 tattcatcgt ggatgtgtgg catccggaac tgacaccaca gcagagacgc agccttccag 2280
262 caatttagca tgaattcga caagcttggg aaactctgga gaga 2324
265 <210> SEQ ID NO: 4
266 <211> LENGTH: 31
267 <212> TYPE: PRT

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Input Set : A:\Rih32d21.app

Output Set: N:\CRF3\10242001\I903216.raw

268 <213> ORGANISM: Artificial Sequence
 270 <220> FEATURE:
 271 <223> OTHER INFORMATION: Description of Artificial Sequence: EGF-like
 272 cysteine-rich repeat
 274 <220> FEATURE:
 275 <221> NAME/KEY: VARIANT
 276 <222> LOCATION: (3)..(5)
 277 <223> OTHER INFORMATION: Wherein any Xaa may be any amino acid
 279 <220> FEATURE:
 280 <221> NAME/KEY: VARIANT
 281 <222> LOCATION: (6)..(7)
 282 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 284 <220> FEATURE:
 285 <221> NAME/KEY: VARIANT
 286 <222> LOCATION: (10)
 287 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 289 <220> FEATURE:
 290 <221> NAME/KEY: VARIANT
 291 <222> LOCATION: (14)
 292 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 294 <220> FEATURE:
 295 <221> NAME/KEY: VARIANT
 296 <222> LOCATION: (17)..(18)
 298 <220> FEATURE:
 299 <221> NAME/KEY: VARIANT
 300 <222> LOCATION: (25)..(26)
 301 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 303 <220> FEATURE:
 304 <221> NAME/KEY: VARIANT
 305 <222> LOCATION: (29)
 306 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 308 <400> SEQUENCE: 4

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 310 1 5 10 15

W--> 312 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys
 313 20 25 30

316 <210> SEQ ID NO: 5

317 <211> LENGTH: 1242

318 <212> TYPE: PRT

319 <213> ORGANISM: Homo sapiens

321 <400> SEQUENCE: 5

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323 1 5 10 15

325 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu

326 20 25 30

328 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu

329 35 40 45

331 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile

332 50 55 60

VERIFICATION SUMMARY

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Input Set : A:\Rih32d21.app

Output Set: N:\CRF3\10242001\I903216.raw

L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4